

attach #10

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SEQUENCE LISTING

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<120> METHODS OF CONFERRING PPO-INHIBITING HERBICIDE RESISTANCE IN PLANTS BY
GENE MANIPULATION

<130> 2185-156P

<140> US 09/331,723

<141> 1999-08-18

<150> PCT/US96/20415

<151> 1996-12-27

<160> 24

<170> PatentIn version 3.0

<210> 1

<211> 47

<212> PRT

<213> Chlamydomonas reinhardtii

<220>

<221> misc_feature

<222> ()..()

<223> Strain CC-407

<220>

<221> PEPTIDE

<222> (1)..(47)

<223> product = porphyric herbicide resistance domain

<400> 1

Ala Ala Glu Ala Leu Gly Ser Phe Asp Tyr Pro Pro Val Gly Ala Val
1 5 10 15

Thr Leu Ser Tyr Pro Leu Ser Ala Val Arg Glu Glu Arg Lys Ala Ser
20 25 30

Asp Gly Ser Val Pro Gly Phe Gly Gln Leu His Pro Arg Thr Gln
35 40 45

<210> 2

<211> 46

<212> PRT

<213> Arabidopsis thaliana

<220>

<221> misc_feature
 <222> ()..()
 <223> ecotype Columbia

<220>
 <221> PEPTIDE
 <222> (1)..(46)
 <223> product = porphyric herbicide resistance domain

<400> 2

Ala	Ala	Asn	Ala	Leu	Ser	Lys	Leu	Tyr	Tyr	Pro	Pro	Val	Ala	Ala	Val
1				5				10					15		
Ser	Ile	Ser	Tyr	Pro	Lys	Glu	Ala	Ile	Arg	Thr	Glu	Cys	Leu	Ile	Asp
			20					25					30		
Gly	Glu	Leu	Lys	Gly	Phe	Gly	Gln	Leu	His	Pro	Arg	Thr	Gln		
		35					40					45			

<210> 3
 <211> 46
 <212> PRT
 <213> Zea mays

<220>
 <221> misc_feature
 <222> ()..()
 <223> Strain B73 inbred

<220>
 <221> PEPTIDE
 <222> (1)..(46)
 <223> product = porphyric herbicide resistance domain

<400> 3

Ala	Ala	Asp	Ala	Leu	Ser	Arg	Phe	Tyr	Tyr	Pro	Pro	Val	Ala	Ala	Val
1				5				10					15		
Thr	Val	Ser	Tyr	Pro	Lys	Glu	Ala	Ile	Arg	Lys	Glu	Cys	Leu	Ile	Asp
			20					25					30		
Gly	Glu	Leu	Gln	Gly	Phe	Gly	Gln	Leu	His	Pro	Arg	Ser	Gln		
		35					40					45			

<210> 4
 <211> 141
 <212> DNA
 <213> Chlamydomonas reinhardtii

<220>
 <221> misc_feature

<222> ()..()
<223> Strain CC-407

<220>
<221> misc_feature
<222> (1)..(141)
<223> encodes porphyrin herbicide resistance domain

<400> 4
gcgcgcgagg ccctgggctc cttcgactac ccgcccgtgg gcgcgcgtgac gctgtcgtac 60
ccgctgagcg ccgtgcggga ggagcgcaag gcctcggacg ggtccgtgcc gggcttcggt 120
cagctgcacc cgcgcacgca g 141

<210> 5
<211> 138
<212> DNA
<213> Arabidopsis thaliana

<220>
<221> misc_feature
<222> ()..()
<223> ecotype Columbia

<220>
<221> misc_feature
<222> (1)..(138)
<223> encodes porphyrin herbicide resistance domain

<400> 5
gctgcaaatg cactctcaaa actatattac ccaccagttg cagcagtatc tatctcgtac 60
ccgaaagaag caatccgaac agaatgtttg atagatggtg aactaaaggg ttttgggcaa 120
ttgcatccac gcacgcaa 138

<210> 6
<211> 138
<212> DNA
<213> Zea mays

<220>
<221> misc_feature
<222> ()..()
<223> Strain B73 inbred

<220>
<221> misc_feature
<222> (1)..(138)

<223> encodes porphyric herbicide resistance domain

<400> 6
gctgcagatg ctctatcaag attctattat ccaccggttg ctgctgtaac tgtttcgtat 60
ccaaaggaag caattagaaa agaatgctta attgatgggg aactccaggg ctttggccag 120
ttgcatccac gtagtcaa 138

<210> 7
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<221> misc_feature
<222> (1)..(36)
<223> Oligonucleotide primer for Arabidopsis thaliana

<400> 7
ctatattacc caccaatggc agcagtatct atctcg 36

<210> 8
<211> 38
<212> DNA
<213> Artificial Sequence

<220>
<221> misc_feature
<222> (1)..(38)
<223> Oligonucleotide primer for Zea mays

<400> 8
gattctatta tccaccgatg gctgctgtaa ctgtttcg 38

<210> 9
<211> 26
<212> PRT
<213> Artificial Sequence

<220>
<221> misc_feature
<222> ()..()
<223> Oligonucleotide primer common to both of A. thaliana and Z. mays
p

<220>
<221> misc_feature
<222> ()..()
<223> "n" residues can be inosine in addition to G, A, T or C; "k" at p

o

<400> 9

Lys Ala Tyr Thr Ala Tyr Cys Cys Asn Cys Cys Asn Ala Thr Gly Gly
1 5 10 15

Ser Asn Gly Cys Asn Gly Thr Asn Trp Ser
20 25

<210> 10

<211> 2573

<212> DNA

<213> Chlamydomonas reinhardtii

<220>

<221> misc_feature

<222> ()..()

<223> Strain RS-3

<220>

<221> misc_feature

<222> (1)..(2573)

<223> encodes protoporphyrinogen oxidase

<400> 10

ctcgagagcg ttggaggaaa tccgtttggc acctgttccg gcttccttgt gtgcacggcc 60
acgtccccct ttcttgctac ccgtccccc ccggctttac tgccccttcc actcctcggc 120
tccatcccgga ttccatccgc tctcctccc ccacctagac tgtctaccgt ctaccagttt 180
cttgggcaat cattaacgta accccgcctc cctgcgctg cccctccctc cctctccccc 240
ccgcacagcc cgcgcgcgcg gaggccctgg gctccttcga ctaccgcgcg atgggcgcgcg 300
tgacgctgtc gtaccgcctg agcgccgtgc gggaggagcg caaggcctcg gacgggtccg 360
tgccggggctt cggtcagctg caccgcgca cgcaggtggg caagtgcgcg cgtgttgcg 420
gcggtgtgtt gcggagggga ggggtgtggg ggttgggggt ggggggtggg gggattggg 480
cgctgggtcg tatccgcgg ttgtatcctc gcgctccct catccattcc ccccttcaac 540
aacacacacg ggcgcacacg caccctcttt gcgcttactt tgtctggtgc tccttaacac 600
actcttcgct tcattttggt gtcttctaac acacacactt gtccacacac agggcatcac 660
cactctgggc accatctaca gtcacagcct gttccccggc cgcgcgccc agggccacat 720
gcgcgcgcgc aactacatcg gcggcaccac caaccgcggc atcgtaacc agaccaccga 780
gcagctggtg gagcaggtgt gtgtgtgggg ggggtggggg ggggcagtgg atttttgggc 840

tgagccccct gagcaaagcg atccaggggg ggccaagccc cccaggattg cccctgtccg	900
tgcgtgcgtg tgtgcctgtg tcgacaaaa gtaccgtact ggcacaaacc gcgagtgcc	960
cgtattatta attgcaatta cctattgtag aaaaatagac ggcagggaaa actcggccgg	1020
agcgagaagc gacctcgtga gtccatggac atcttgactt tcttcagttc gcgagtatag	1080
ctctcggccc cttaaatact taccatccatg tatcaaaaca tgtcgacgac aagcgtcttg	1140
gggcaagaat gtcgaaattg tttgcaacag ccaaaccatg cgtccccgag ccttacatgt	1200
gtcgcggccc gggatcccgc gcccgagccc ggctagccct ttgcggtgct tgagtgggat	1260
gtgggtgagg tgcatttggg atatcatgga ccgtgaagtg gcgtgggtaa ggtggcgtgg	1320
cgtggcgggg acagggcatg tcggtgcctc ggcacagcgt tggcctagtg gccagtccc	1380
ctggatgggc ttgcaagggt gctgttcatg tcgccggtgc ccatcgtcac atccccctgc	1440
gctacatggg gctcagccca ttttcagct gtacaaagct gacaccctt gttgtgtggc	1500
gtottggacc cgtgttgctt cggagctggc cagaaccccc tgtgggcaca cacacgcaca	1560
cacacacaca cacacacaca cacacacaca cacacacaca cacacacaca cacacacaca	1620
cacacacaca cacacacaca cacacacaca cacacacaca cacattttcg tcctgcagcc	1680
cogaaccccc cgcgccgttc cacgtcttcc acctgccgca ccccccccc tgccgcacgc	1740
ctgctctcac cgctctccc cccaccccat ctccctgcag gtggacaagg acctgcgcaa	1800
catggtcatc aagcccgcgc cgcccaagcc ccgtgtggtg ggcgtgcgcg tgtggccgcg	1860
cgccatcccg caggtgtgag ggcgcagcag ccggagggat gggctagatc ctagtttctc	1920
aaagagctct acagccctat aacctcgacc tgcgaccttc gacctgataa cctggctgcc	1980
ccctcccaac ctagccacct ctccccggat ttgggttcac tcggttgact tgcttttggg	2040
ttctggaatc aacttcacct gttgtatact ttgctgcact tctctgtacc actctttgca	2100
ttaggttcgg tttagtttgg gctgcatgtg taaccctcc tccccgccct gccacctgca	2160
gttcaacctg ggccacctgg agcagctgga caaggcgcgc aaggcgtgg acgcggcggg	2220
gctgcagggc gtgcacctgg ggggcaacta cgtcagcggg gagcgcgtgg gcagcagcag	2280
cagcaggaag aggggagggg aggggagggg aggggtacaag gaggagggtg agcaggaggt	2340
gggtgctaagg cgcaaagcaa ggcggtgttg tatcctcatt gactgaaacc gggaaacca	2400
gcatgaacaa gaggtcaggg gactgcaagg agcggaggct acatgtatga ctacccccga	2460
cgcgggcgat gattccttga ctattgggac ctatttcgtt gggctcgggc acatgacccc	2520
cctggcccct tcgctgtatg gtgcccagcc gcccgccgc cccccccca cac	2573

<210> 11
 <211> 1704
 <212> DNA
 <213> Arabidopsis thaliana

<220>
 <221> misc_feature
 <222> ()..()
 <223> ecotype Columbia

<220>
 <221> CDS
 <222> (16)..(1629)
 <223> product = protoporphyrinogen oxidase

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 Met Glu Leu Ser Leu Leu Arg Pro Thr Thr Gln Ser
 1 5 10

ctt ctt ccg tcg ttt tcg aag ccc aat ctc cga tta aat gtt tat aag 99
 Leu Leu Pro Ser Phe Ser Lys Pro Asn Leu Arg Leu Asn Val Tyr Lys
 15 20 25

cct ctt aga ctc cgt tgt tca gtg gcc ggt gga cca acc gtc gga tct 147
 Pro Leu Arg Leu Arg Cys Ser Val Ala Gly Gly Pro Thr Val Gly Ser
 30 35 40

tca aaa atc gaa ggc gga gga ggc acc acc atc acg acg gat tgt gtg 195
 Ser Lys Ile Glu Gly Gly Gly Gly Thr Thr Ile Thr Thr Asp Cys Val
 45 50 55 60

att gtc ggc gga ggt att agt ggt ctt tgc atc gct cag gcg ctt gct 243
 Ile Val Gly Gly Gly Ile Ser Gly Leu Cys Ile Ala Gln Ala Leu Ala
 65 70 75

act aag cat cct gat gct gct ccg aat tta att gtg acc gag gct aag 291
 Thr Lys His Pro Asp Ala Ala Pro Asn Leu Ile Val Thr Glu Ala Lys
 80 85 90

gat cgt gtt gga ggc aac att atc act cgt gaa gag aat ggt ttt ctc 339
 Asp Arg Val Gly Gly Asn Ile Ile Thr Arg Glu Glu Asn Gly Phe Leu
 95 100 105

tgg gaa gaa ggt ccc aat agt ttt caa ccg tct gat cct atg ctc act 387
 Trp Glu Glu Gly Pro Asn Ser Phe Gln Pro Ser Asp Pro Met Leu Thr
 110 115 120

atg gtg gta gat agt ggt ttg aag gat gat ttg gtg ttg gga gat cct 435
 Met Val Val Asp Ser Gly Leu Lys Asp Asp Leu Val Leu Gly Asp Pro
 125 130 135 140

act gcg cca agg ttt gtg ttg tgg aat ggg aaa ttg agg ccg gtt cca 483

Thr	Ala	Pro	Arg	Phe	Val	Leu	Trp	Asn	Gly	Lys	Leu	Arg	Pro	Val	Pro		
				145					150					155			
tcg	aag	cta	aca	gac	tta	ccg	ttc	ttt	gat	ttg	atg	agt	att	ggg	ggg	531	
Ser	Lys	Leu	Thr	Asp	Leu	Pro	Phe	Phe	Asp	Leu	Met	Ser	Ile	Gly	Gly		
			160					165					170				
aag	att	aga	gct	ggg	ttt	ggg	gca	ctt	ggc	att	cga	ccg	tca	cct	cca	579	
Lys	Ile	Arg	Ala	Gly	Phe	Gly	Ala	Leu	Gly	Ile	Arg	Pro	Ser	Pro	Pro		
		175					180					185					
ggg	cgt	gaa	gaa	tct	gtg	gag	gag	ttt	gta	cgg	cgt	aac	ctc	ggg	gat	627	
Gly	Arg	Glu	Glu	Ser	Val	Glu	Glu	Phe	Val	Arg	Arg	Asn	Leu	Gly	Asp		
	190					195					200						
gag	gtt	ttt	gag	cgc	ctg	att	gaa	ccg	ttt	tgt	tca	ggg	gtt	tat	gct	675	
Glu	Val	Phe	Glu	Arg	Leu	Ile	Glu	Pro	Phe	Cys	Ser	Gly	Val	Tyr	Ala		
205					210				215						220		
ggg	gat	cct	tca	aaa	ctg	agc	atg	aaa	gca	gcg	ttt	ggg	aag	gtt	tgg	723	
Gly	Asp	Pro	Ser	Lys	Leu	Ser	Met	Lys	Ala	Ala	Phe	Gly	Lys	Val	Trp		
				225					230					235			
aaa	cta	gag	caa	aat	ggg	gga	agc	ata	ata	ggg	ggg	act	ttt	aag	gca	771	
Lys	Leu	Glu	Gln	Asn	Gly	Gly	Ser	Ile	Ile	Gly	Gly	Thr	Phe	Lys	Ala		
			240					245					250				
att	cag	gag	agg	aaa	aac	gct	ccc	aag	gca	gaa	cga	gac	ccg	cgc	ctg	819	
Ile	Gln	Glu	Arg	Lys	Asn	Ala	Pro	Lys	Ala	Glu	Arg	Asp	Pro	Arg	Leu		
		255					260					265					
cca	aaa	cca	cag	ggc	caa	aca	gtt	ggg	tct	ttc	agg	aag	gga	ctt	cga	867	
Pro	Lys	Pro	Gln	Gly	Gln	Thr	Val	Gly	Ser	Phe	Arg	Lys	Gly	Leu	Arg		
		270				275					280						
atg	ttg	cca	gaa	gca	ata	tct	gca	aga	tta	ggg	agc	aaa	gtt	aag	ttg	915	
Met	Leu	Pro	Glu	Ala	Ile	Ser	Ala	Arg	Leu	Gly	Ser	Lys	Val	Lys	Leu		
285					290				295						300		
tct	tgg	aag	ctc	tca	ggg	atc	act	aag	ctg	gag	agc	gga	gga	tac	aac	963	
Ser	Trp	Lys	Leu	Ser	Gly	Ile	Thr	Lys	Leu	Glu	Ser	Gly	Gly	Tyr	Asn		
			305						310					315			
tta	aca	tat	gag	act	cca	gat	ggg	tta	gtt	tcc	gtg	cag	agc	aaa	agt	1011	
Leu	Thr	Tyr	Glu	Thr	Pro	Asp	Gly	Leu	Val	Ser	Val	Gln	Ser	Lys	Ser		
			320				325						330				
gtt	gta	atg	acg	gtg	cca	tct	cat	gtt	gca	agt	ggg	ctc	ttg	cgc	cct	1059	
Val	Val	Met	Thr	Val	Pro	Ser	His	Val	Ala	Ser	Gly	Leu	Leu	Arg	Pro		
		335					340					345					
ctt	tct	gaa	tct	gct	gca	aat	gca	ctc	tca	aaa	cta	tat	tac	cca	cca	1107	
Leu	Ser	Glu	Ser	Ala	Ala	Asn	Ala	Leu	Ser	Lys	Leu	Tyr	Tyr	Pro	Pro		
		350				355					360						
gtt	gca	gca	gta	tct	atc	tcg	tac	ccg	aaa	gaa	gca	atc	cga	aca	gaa	1155	
Val	Ala	Ala	Val	Ser	Ile	Ser	Tyr	Pro	Lys	Glu	Ala	Ile	Arg	Thr	Glu		

365	370	375	380	
tgt ttg ata gat ggt gaa cta aag ggt ttt ggg caa ttg cat cca cgc				1203
Cys Leu Ile Asp Gly Glu Leu Lys Gly Phe Gly Gln Leu His Pro Arg	385	390	395	
acg caa gga gtt gaa aca tta gga act atc tac agc tcc tca ctc ttt				1251
Thr Gln Gly Val Glu Thr Leu Gly Thr Ile Tyr Ser Ser Ser Leu Phe	400	405	410	
cca aat cgc gca ccg ccc gga aga att ttg ctg ttg aac tac att ggc				1299
Pro Asn Arg Ala Pro Pro Gly Arg Ile Leu Leu Leu Asn Tyr Ile Gly	415	420	425	
ggg tct aca aac acc gga att ctg tcc aag tct gaa ggt gag tta gtg				1347
Gly Ser Thr Asn Thr Gly Ile Leu Ser Lys Ser Glu Gly Glu Leu Val	430	435	440	
gaa gca gtt gac aga gat ttg agg aaa atg cta att aag cct aat tcg				1395
Glu Ala Val Asp Arg Asp Leu Arg Lys Met Leu Ile Lys Pro Asn Ser	445	450	455	460
acc gat cca ctt aaa tta gga gtt agg gta tgg cct caa gcc att cct				1443
Thr Asp Pro Leu Lys Leu Gly Val Arg Val Trp Pro Gln Ala Ile Pro	465	470	475	
cag ttt cta gtt ggt cac ttt gat atc ctt gac acg gct aaa tca tct				1491
Gln Phe Leu Val Gly His Phe Asp Ile Leu Asp Thr Ala Lys Ser Ser	480	485	490	
cta acg tct tcg ggc tac gaa ggg cta ttt ttg ggt ggc aat tac gtc				1539
Leu Thr Ser Ser Gly Tyr Glu Gly Leu Phe Leu Gly Gly Asn Tyr Val	495	500	505	
gct ggt gta gcc tta ggc cgg tgt gta gaa ggc gca tat gaa acc gcg				1587
Ala Gly Val Ala Leu Gly Arg Cys Val Glu Gly Ala Tyr Glu Thr Ala	510	515	520	
att gag gtc aac aac ttc atg tca cgg tac gct tac aag taa				1629
Ile Glu Val Asn Asn Phe Met Ser Arg Tyr Ala Tyr Lys	525	530	535	
atgtaaaaca ttaaattctcc cagcttgcggt gagttttatt aaatatatttg agatatccaa				1689
aaaaaaaaaaaa aaaaa				1704

<210> 12
 <211> 537
 <212> PRT
 <213> Arabidopsis thaliana

 <220>
 <221> misc_feature
 <222> ()..()
 <223> ecotype Columbia

<400> 12

Met Glu Leu Ser Leu Leu Arg Pro Thr Thr Gln Ser Leu Leu Pro Ser
1 5 10 15

Phe Ser Lys Pro Asn Leu Arg Leu Asn Val Tyr Lys Pro Leu Arg Leu
20 25 30

Arg Cys Ser Val Ala Gly Gly Pro Thr Val Gly Ser Ser Lys Ile Glu
35 40 45

Gly Gly Gly Gly Thr Thr Ile Thr Thr Asp Cys Val Ile Val Gly Gly
50 55 60

Gly Ile Ser Gly Leu Cys Ile Ala Gln Ala Leu Ala Thr Lys His Pro
65 70 75 80

Asp Ala Ala Pro Asn Leu Ile Val Thr Glu Ala Lys Asp Arg Val Gly
85 90 95

Gly Asn Ile Ile Thr Arg Glu Glu Asn Gly Phe Leu Trp Glu Glu Gly
100 105 110

Pro Asn Ser Phe Gln Pro Ser Asp Pro Met Leu Thr Met Val Val Asp
115 120 125

Ser Gly Leu Lys Asp Asp Leu Val Leu Gly Asp Pro Thr Ala Pro Arg
130 135 140

Phe Val Leu Trp Asn Gly Lys Leu Arg Pro Val Pro Ser Lys Leu Thr
145 150 155 160

Asp Leu Pro Phe Phe Asp Leu Met Ser Ile Gly Gly Lys Ile Arg Ala
165 170 175

Gly Phe Gly Ala Leu Gly Ile Arg Pro Ser Pro Pro Gly Arg Glu Glu
180 185 190

Ser Val Glu Glu Phe Val Arg Arg Asn Leu Gly Asp Glu Val Phe Glu
195 200 205

Arg Leu Ile Glu Pro Phe Cys Ser Gly Val Tyr Ala Gly Asp Pro Ser
210 215 220

Lys Leu Ser Met Lys Ala Ala Phe Gly Lys Val Trp Lys Leu Glu Gln
 225 230 235 240

Asn Gly Gly Ser Ile Ile Gly Gly Thr Phe Lys Ala Ile Gln Glu Arg
 245 250 255

Lys Asn Ala Pro Lys Ala Glu Arg Asp Pro Arg Leu Pro Lys Pro Gln
 260 265 270

Gly Gln Thr Val Gly Ser Phe Arg Lys Gly Leu Arg Met Leu Pro Glu
 275 280 285

Ala Ile Ser Ala Arg Leu Gly Ser Lys Val Lys Leu Ser Trp Lys Leu
 290 295 300

Ser Gly Ile Thr Lys Leu Glu Ser Gly Gly Tyr Asn Leu Thr Tyr Glu
 305 310 315 320

Thr Pro Asp Gly Leu Val Ser Val Gln Ser Lys Ser Val Val Met Thr
 325 330 335

Val Pro Ser His Val Ala Ser Gly Leu Leu Arg Pro Leu Ser Glu Ser
 340 345 350

Ala Ala Asn Ala Leu Ser Lys Leu Tyr Tyr Pro Pro Val Ala Ala Val
 355 360 365

Ser Ile Ser Tyr Pro Lys Glu Ala Ile Arg Thr Glu Cys Leu Ile Asp
 370 375 380

Gly Glu Leu Lys Gly Phe Gly Gln Leu His Pro Arg Thr Gln Gly Val
 385 390 395 400

Glu Thr Leu Gly Thr Ile Tyr Ser Ser Ser Leu Phe Pro Asn Arg Ala
 405 410 415

Pro Pro Gly Arg Ile Leu Leu Leu Asn Tyr Ile Gly Gly Ser Thr Asn
 420 425 430

Thr Gly Ile Leu Ser Lys Ser Glu Gly Glu Leu Val Glu Ala Val Asp
 435 440 445

Arg Asp Leu Arg Lys Met Leu Ile Lys Pro Asn Ser Thr Asp Pro Leu
 450 455 460

Lys Leu Gly Val Arg Val Trp Pro Gln Ala Ile Pro Gln Phe Leu Val
 465 470 475 480

Gly His Phe Asp Ile Leu Asp Thr Ala Lys Ser Ser Leu Thr Ser Ser
 485 490 495

Gly Tyr Glu Gly Leu Phe Leu Gly Gly Asn Tyr Val Ala Gly Val Ala
 500 505 510

Leu Gly Arg Cys Val Glu Gly Ala Tyr Glu Thr Ala Ile Glu Val Asn
 515 520 525

Asn Phe Met Ser Arg Tyr Ala Tyr Lys
 530 535

<210> 13
 <211> 1698
 <212> DNA
 <213> Zea mays

<220>
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 <222> ()..()
 <223> Strain B73 inbred

<220>
 <221> CDS
 <222> (2)..(1453)
 <223> product = protoporphyrinogen oxidase

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 Asn Ser Ala Asp Cys Val Val Val Gly Gly Ile Ser Gly Leu Cys
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 acc gcg cag gcg ctg gcc acg cgg cac ggc gtc ggg gac gtg ctt gtc 97
 Thr Ala Gln Ala Leu Ala Thr Arg His Gly Val Gly Asp Val Leu Val
 20 25 30
 acg gag gcc cgc gcc cgc ccc ggc ggc aac att acc acc gtc gag cgc 145
 Thr Glu Ala Arg Ala Arg Pro Gly Gly Asn Ile Thr Thr Val Glu Arg
 35 40 45
 ccc gag gaa ggg tac ctc tgg gag gag ggt ccc aac agc ttc cag ccc 193
 Pro Glu Glu Gly Tyr Leu Trp Glu Glu Gly Pro Asn Ser Phe Gln Pro
 50 55 60

tcc gac ccc gtt ctc acc atg gcc gtg gac agc gga ctg aag gat gac	241
Ser Asp Pro Val Leu Thr Met Ala Val Asp Ser Gly Leu Lys Asp Asp	
65 70 75 80	
ttg gtt ttt ggg gac cca aac gcg ccg cgt ttc gtg ctg tgg gag ggg	289
Leu Val Phe Gly Asp Pro Asn Ala Pro Arg Phe Val Leu Trp Glu Gly	
85 90 95	
aag ctg agg ccc gtg cca tcc aag ccc gcc gac ctc ccg ttc ttc gat	337
Lys Leu Arg Pro Val Pro Ser Lys Pro Ala Asp Leu Pro Phe Phe Asp	
100 105 110	
ctc atg agc atc cca ggg aag ctc agg gcc ggt cta ggc gcg ctt ggc	385
Leu Met Ser Ile Pro Gly Lys Leu Arg Ala Gly Leu Gly Ala Leu Gly	
115 120 125	
atc cgc ccg cct cct cca ggc cgc gaa gag tca gtg gag gag ttc gtg	433
Ile Arg Pro Pro Pro Pro Gly Arg Glu Glu Ser Val Glu Glu Phe Val	
130 135 140	
cgc cgc aac ctc ggt gct gag gtc ttt gag cgc ctc att gag cct ttc	481
Arg Arg Asn Leu Gly Ala Glu Val Phe Glu Arg Leu Ile Glu Pro Phe	
145 150 155 160	
tgc tca ggt gtc tat gct ggt gat cct tct aag ctc agc atg aag gct	529
Cys Ser Gly Val Tyr Ala Gly Asp Pro Ser Lys Leu Ser Met Lys Ala	
165 170 175	
gca ttt ggg aag gtt tgg cgg ttg gaa gaa act gga ggt agt att att	577
Ala Phe Gly Lys Val Trp Arg Leu Glu Glu Thr Gly Gly Ser Ile Ile	
180 185 190	
ggt gga acc atc aag aca att cag gag agg agc aag aat cca aaa cca	625
Gly Gly Thr Ile Lys Thr Ile Gln Glu Arg Ser Lys Asn Pro Lys Pro	
195 200 205	
ccg agg gat gcc cgc ctt ccg aag cca aaa ggg cag aca gtt gca tct	673
Pro Arg Asp Ala Arg Leu Pro Lys Pro Lys Gly Gln Thr Val Ala Ser	
210 215 220	
ttc agg aag ggt ctt gcc atg ctt cca aat gcc att aca tcc agc ttg	721
Phe Arg Lys Gly Leu Ala Met Leu Pro Asn Ala Ile Thr Ser Ser Leu	
225 230 235 240	
ggt agt aaa gtc aaa cta tca tgg aaa ctc acg agc att aca aaa tca	769
Gly Ser Lys Val Lys Leu Ser Trp Lys Leu Thr Ser Ile Thr Lys Ser	
245 250 255	
gat gac aag gga tat gtt ttg gag tat gaa acg cca gaa ggg gtt gtt	817
Asp Asp Lys Gly Tyr Val Leu Glu Tyr Glu Thr Pro Glu Gly Val Val	
260 265 270	
tcg gtg cag gct aaa agt gtt atc atg act att cca tca tat gtt gct	865
Ser Val Gln Ala Lys Ser Val Ile Met Thr Ile Pro Ser Tyr Val Ala	
275 280 285	

agc aac att ttg cgt cca ctt tca agc gat gct gca gat gct cta tca Ser Asn Ile Leu Arg Pro Leu Ser Ser Asp Ala Ala Asp Ala Leu Ser 290 295 300	913
aga ttc tat tat cca ccg gtt gct gct gta act gtt tcg tat cca aag Arg Phe Tyr Tyr Pro Pro Val Ala Ala Val Thr Val Ser Tyr Pro Lys 305 310 315 320	961
gaa gca att aga aaa gaa tgc tta att gat ggg gaa ctc cag ggc ttt Glu Ala Ile Arg Lys Glu Cys Leu Ile Asp Gly Glu Leu Gln Gly Phe 325 330 335	1009
ggc cag ttg cat cca cgt agt caa gga gtt gag aca tta gga aca ata Gly Gln Leu His Pro Arg Ser Gln Gly Val Glu Thr Leu Gly Thr Ile 340 345 350	1057
tac agt tcc tca ctc ttt cca aat cgt gct cct gac ggt agg gtg tta Tyr Ser Ser Ser Leu Phe Pro Asn Arg Ala Pro Asp Gly Arg Val Leu 355 360 365	1105
ctt cta aac tac ata gga ggt gct aca aac aca gga att gtt tcc aag Leu Leu Asn Tyr Ile Gly Gly Ala Thr Asn Thr Gly Ile Val Ser Lys 370 375 380	1153
act gaa agt gag ctg gtc gaa gca gtt gac cgt gac ctc cga aaa atg Thr Glu Ser Glu Leu Val Glu Ala Val Asp Arg Asp Leu Arg Lys Met 385 390 395 400	1201
ctt ata aat tct aca gca gtg gac cct tta gtc ctt ggt gtt cga gtt Leu Ile Asn Ser Thr Ala Val Asp Pro Leu Val Leu Gly Val Arg Val 405 410 415	1249
tgg cca caa gcc ata cct cag ttc ctg gta gga cat ctt gat ctt ctg Trp Pro Gln Ala Ile Pro Gln Phe Leu Val Gly His Leu Asp Leu Leu 420 425 430	1297
gaa gcc gca aaa gct gcc ctg gac cga ggt ggc tac gat ggg ctg ttc Glu Ala Ala Lys Ala Ala Leu Asp Arg Gly Gly Tyr Asp Gly Leu Phe 435 440 445	1345
cta gga ggg aac tat gtt gca gga gtt gcc ctg ggc aga tgc gtt gag Leu Gly Gly Asn Tyr Val Ala Gly Val Ala Leu Gly Arg Cys Val Glu 450 455 460	1393
ggc gcg tat gaa agt gcc tcg caa ata tct gac ttc ttg acc aag tat Gly Ala Tyr Glu Ser Ala Ser Gln Ile Ser Asp Phe Leu Thr Lys Tyr 465 470 475 480	1441
gcc tac aag tga tgaaagaagt ggagcgctac ttgccaatcg tttatgttgc Ala Tyr Lys	1493
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1698

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<211> 483
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<213> Zea mays

<220>
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<223> Strain B73 inbred

<400> 14

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35 40 45

Pro Glu Glu Gly Tyr Leu Trp Glu Glu Gly Pro Asn Ser Phe Gln Pro
50 55 60

Ser Asp Pro Val Leu Thr Met Ala Val Asp Ser Gly Leu Lys Asp Asp
65 70 75 80

Leu Val Phe Gly Asp Pro Asn Ala Pro Arg Phe Val Leu Trp Glu Gly
85 90 95

Lys Leu Arg Pro Val Pro Ser Lys Pro Ala Asp Leu Pro Phe Phe Asp
100 105 110

Leu Met Ser Ile Pro Gly Lys Leu Arg Ala Gly Leu Gly Ala Leu Gly
115 120 125

Ile Arg Pro Pro Pro Pro Gly Arg Glu Glu Ser Val Glu Glu Phe Val
130 135 140

Arg Arg Asn Leu Gly Ala Glu Val Phe Glu Arg Leu Ile Glu Pro Phe
145 150 155 160

Cys Ser Gly Val Tyr Ala Gly Asp Pro Ser Lys Leu Ser Met Lys Ala

165	170	175
Ala Phe Gly Lys Val Trp Arg Leu Glu Glu Thr Gly Gly Ser Ile Ile 180 185 190		
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Phe Arg Lys Gly Leu Ala Met Leu Pro Asn Ala Ile Thr Ser Ser Leu 225 230 235 240		
Gly Ser Lys Val Lys Leu Ser Trp Lys Leu Thr Ser Ile Thr Lys Ser 245 250 255		
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Arg Phe Tyr Tyr Pro Pro Val Ala Ala Val Thr Val Ser Tyr Pro Lys 305 310 315 320		
Glu Ala Ile Arg Lys Glu Cys Leu Ile Asp Gly Glu Leu Gln Gly Phe 325 330 335		
Gly Gln Leu His Pro Arg Ser Gln Gly Val Glu Thr Leu Gly Thr Ile 340 345 350		
Tyr Ser Ser Ser Leu Phe Pro Asn Arg Ala Pro Asp Gly Arg Val Leu 355 360 365		
Leu Leu Asn Tyr Ile Gly Gly Ala Thr Asn Thr Gly Ile Val Ser Lys 370 375 380		
Thr Glu Ser Glu Leu Val Glu Ala Val Asp Arg Asp Leu Arg Lys Met 385 390 395 400		

Leu Ile Asn Ser Thr Ala Val Asp Pro Leu Val Leu Gly Val Arg Val
405 410 415

Trp Pro Gln Ala Ile Pro Gln Phe Leu Val Gly His Leu Asp Leu Leu
420 425 430

Glu Ala Ala Lys Ala Ala Leu Asp Arg Gly Gly Tyr Asp Gly Leu Phe
435 440 445

Leu Gly Gly Asn Tyr Val Ala Gly Val Ala Leu Gly Arg Cys Val Glu
450 455 460

Gly Ala Tyr Glu Ser Ala Ser Gln Ile Ser Asp Phe Leu Thr Lys Tyr
465 470 475 480

Ala Tyr Lys

<210> 15
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<221> misc_feature
<222> (1)..(18)
<223> Oligonucleotide primer 1A for Chlamydomonas reinhardtii

<400> 15
ccgtctacca gtttcttg 18

<210> 16
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<221> misc_feature
<222> (1)..(19)
<223> Oligonucleotide primer 1B for Chlamydomonas reinhardtii

<400> 16
atacaaccgc gggatacga 19

<210> 17

<211> 17
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> misc_feature
 <222> (1)..(17)
 <223> Oligonucleotide primer 2A for Chlamydomonas reinhardtii

<400> 17
 actttgtctg gtgctcc 17

<210> 18
 <211> 17
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 <213> Artificial Sequence

<220>
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 <222> (1)..(17)
 <223> Oligonucleotide primer 2B for Chlamydomonas reinhardtii

<400> 18
 tggatcgctt tgctcag 17

<210> 19
 <211> 3381
 <212> DNA
 <213> Chlamydomonas reinhardtii

<220>
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<210> 20

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<221> misc_feature

<222> (1)..(18)

<223> Oligonucleotide primer 3A for Chlamydomonas reinhardtii

<400> 20
ttccacgtct tccacctg 18

<210> 21
<211> 17
<212> DNA
<213> Artificial Sequence

<220>
<221> misc_feature
<222> (1)..(17)
<223> Oligonucleotide primer 3B for Chlamydomonas reinhardtii

<400> 21
ctaggatcta gcccatc 17

<210> 22
<211> 18
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<223> Oligonucleotide primer 4A for Chlamydomonas reinhardtii

<400> 22
ctgcatgtgt aaccctc 18

<210> 23
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<220>
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<222> (1)..(18)
<223> Oligonucleotide primer 4B for Chlamydomonas reinhardtii

<400> 23
gacctcttgt tcatgctg 18

<210> 24
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17